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GAATTCCTGCAGCTCAGCAGCCGCCAGAGCAGGACGAACCGCCAATCGCAAGGCACC
1 -----+-----+-----+-----+-----+-----+ 60
CTTAAGGACGTCGAGTCGTTCGGCGGCGGTCTCGTCCTGCTTGGCGGTTAGCGTTCCTGG

TCTGAGAACTTCAGGATGCAGATGTCTCCAGCCCTCACCTGCCTAGTCCTGGGCCTGGCC
61 -----+-----+-----+-----+-----+-----+ 120
AGACTCTTGAAAGTCCTACGTCTACAGAGGTTCGGGAGTGGACGGATCAGGACCCGGACCGG

aa M Q M S P A L T C L V L G L A -
| Signal Peptide
CTGTCTTTGGTGAAGGGTCTGCTGTGCACCATCCCCCATCTACGTGGCCACCTGGCC
121 -----+-----+-----+-----+-----+-----+ 180
GAACAGAAACCACCTCCAGACGACCGTGGTAGGGGGTAGGATGCACCGGGTGGACCGG

aa L V F G E G S A | V H H P P S Y V A H L A 12
Start Mature Protein
TCAGACTTCGGGGTGAGGGTGTTCAGCAGGTGGCGCAGGCCTCCAAGGACCGCAACGTG
181 -----+-----+-----+-----+-----+-----+ 240
AGTCTGAAGCCCCACTCCACAAAGTCGTCCACCGCGTCCGGAGGTTCTGGCGTTGCAC

aa S D F G V R V F Q Q V A Q A S K D R N V 32
GTTTCTCACCCTATGGGGTGGCCTCGGTGTTGGCCATGCTCCAGCTGACAACAGGAGGA
241 -----+-----+-----+-----+-----+-----+ 300
CAAAAGAGTGGGATACCCACCGGAGCCCAACCGGTACGAGGTGACTGTTGTCTCTCT

aa V F S P Y G V A S V L A M L Q L T T G G 52
GAAACCCAGCAGCAGATTCAAGCAGCTATGGGATTCAAGATTGATGACAAGGGCATGGCC
301 -----+-----+-----+-----+-----+-----+ 360
CTTTGGGTCGTCTAGTTCGTTCGATACCCTAAGTTCTAACTACTGTTCCCGTACCGG

aa E T Q Q Q I Q A A M G F K I D D K G M A 72
CCCCCCTCCGGCATCTGTACAAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGC
361 -----+-----+-----+-----+-----+-----+ 420
GGGCGGGAGGCCGTAGACATGTTCTCGAGTACCCCGGTACCTTGTTCTACTCTAGTCG

aa P A L R H L Y K E L M G P W N K D E I S 92
ACCACAGACGCGATCTTCGTCCAGCGGGATCTAAGCTGGTCCAGGGCTTCATGCCCCAC
421 -----+-----+-----+-----+-----+-----+ 480
TGGTGTCTGCGCTAGAAGCAGGTTCGCCCTAGACTTCGACCAGGTCCCGAAGTACGGGGTG

aa T T D A I F V Q R D L K L V Q G F M P H 112
TTCTTCAGGCTGTTCCGGAGCACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCC
481 -----+-----+-----+-----+-----+-----+ 540
AAGAAGTCCGACAAGGCCTCGTGCCAGTTCGTTACCTGAAAAGTCTCCACCTCTCTCGG

aa F F R L F R S T V K Q V D F S E V E R A 132
AGATTCATCATCAATGACTGGGTGAAGACACACAAAAGGTATGATCAGCAACTTGCTT
541 -----+-----+-----+-----+-----+-----+ 600
TCTAAGTAGTAGTTACTGACCCACTTCTGTGTGTGTTTCCATACTAGTCGTTGAACGAA

aa R F I I N D W V K T H T K G M I S N L L 152

FIG. 1A

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GGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGGTGAATGCCCTCTACTTCAAC
601 -----+-----+-----+-----+-----+-----+ 660
CCCTTTCTCTCGGCACCTGGTTCGACTGTGCCGACCACGACCACTTACGGGAGATGAAGTTG
aa G K G A V D Q L T R L V L V N A L Y F N 172

GGCCAGTGGAAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCGCTCTTCCACAAATCA
661 -----+-----+-----+-----+-----+-----+ 720
CCGGTCACCTTCTGAGGGAAGGGGCTGAGGTCGTGGGTGGCGGCGGAGAAGGTGTTTAGT
aa G Q W K T P F P D S S T H R R L F H K S 192

GACGGCAGCACTGTCTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAG
721 -----+-----+-----+-----+-----+-----+ 780
CTGCCGTCGTGACAGAGACACGGGTACTACCGAGTCTGGTTGTTCAAGTTGATATGACTC
aa D G S T V S V P M M A Q T N K F N Y T E 212

TTCACCACGCCCGATGGCCATTACTACGACATCCTGGAAGTGCCTTACCACGGGGACACC
781 -----+-----+-----+-----+-----+-----+ 840
AAGTGGTGCGGGCTACCGGTAATGATGCTGTAGGACCTTGACGGGATGGTGGCCCTGTGG
aa F T T P D G H Y Y D I L E L P Y H G D T 232

CTCAGCATGTTTCATTGCTGCCCCCTTATGAAAAAGAGGTGCCTCTCTCTGCCCTCACCAAC
841 -----+-----+-----+-----+-----+-----+ 900
GAGTCGTACAAGTAACGACGGGGAATACTTTTTCTCCACGGAGAGAGACGGGAGTGGTTG
aa L S M F I A A P Y E K E V P L S A L T N 252

ATTCTGAGTGCCCGAGCTCATCAGCCACTGGAAGGCAACATGACCAGGCTGCCCCGCCTC
901 -----+-----+-----+-----+-----+-----+ 960
TAAGACTCACGGGTCGAGTAGTCGGTGACCTTTCCGTTGTACTGGTCCGACGGGGCGGAG
aa I L S A Q L I S H W K G N M T R L P R L 272

CTGGTTCTGCCCAAGTTCTCCCTGGAGACTGAAGTCGACCTCAGGAAGCCCCCTAGAGAAC
961 -----+-----+-----+-----+-----+-----+ 1020
GACCAAGACGGGTTCAAGAGGGACCTCTGACTTCAGCTGGAGTCCTTCGGGGATCTCTTG
aa L V L P K F S L E T E V D L R K P L E N 292

CTGGGAATGACCGACATGTTTCAGACAGTTTCAGGCTGACTTCACGAGTCTTTCAGACCAA
1021 -----+-----+-----+-----+-----+-----+ 1080
GACCCCTTACTGGCTGTACAAGTCGTCAAAGTCCGACTGAAGTGCTCAGAAAGTCTGGTT
aa L G M T D M F R Q F Q A D F T S L S D Q 312

GAGCCTCTCCACGTCGCGCAGGCGCTGCAGAAAGTGAAGATCGAGGTGAACGAGAGTGGC
1081 -----+-----+-----+-----+-----+-----+ 1140
CTCGGAGAGGTGCAGCGGCTCCGCGACGCTTTCACTTCTAGCTCCACTTGCTCTCACCG
aa E P L E V A Q A L Q K V K I E V N E S G 332

ACGGTGGCCTCCTCATCCACAGCTGTCTAGTCTCAGCCCGCATGGCCCCCGAGGAGATC
1141 -----+-----+-----+-----+-----+-----+ 1200
TGCCACCGGAGGAGTAGGTGTCGACAGTATCAGAGTCGGGCGTACCGGGGGCTCCTCTAG
aa T V A S S S T A V I V S A R M A P E E I 352

ATCATGGACAGACCCTTCCTCTTTGTGGTCCGGCACAACCCACAGGAACAGTCCTTTTC
1201 -----+-----+-----+-----+-----+-----+ 1260
TAGTACCTGTCTGGGAAGGAGAAACACCAAGCCGCTGTTGGGGTGTCTTGTTCAGGAAAAG
aa I M D R P F L F V V R H N P T G T V L F 372

FIG. 1B

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ATGGGCCAAGTGTATGGAACCCCTGACCCTGGGGAAAGACGCCTTCATCTGGGACAAACTG
1261 -----+-----+-----+-----+-----+-----+ 1320
TACCCGGTTCACTACCTTGGGACTGGGACCCCTTTCTGCGGAAGTAGACCCTGTTTTGAC
M G Q V M E P * 379
GAGATGCATCGGGAAAGAAGAACTCCGAAGAAAAGAATTTTAGTGTTAATGACTCTTTC
1321 -----+-----+-----+-----+-----+-----+ 1380
CTCTACGTAGCCCTTTCTTCTTTGAGGCTTCTTTTCTTAAATCACAACTACTGAGAAAG
TGAGGAAGAGAAGACATTTGCCTTTTGTAAAAGATGGTAAACCAGATCTGTCTCCAAG
1381 -----+-----+-----+-----+-----+-----+ 1440
ACTTCCTTCTCTCTGTAAACGGAAACAATTTTCTACCATTGGTCTAGACAGAGGTTT
ACCTTGGCCTCTCCTTGGAGGACCTTTAGGTCAAACCTCCCTAGTCTCCACCTGAGACCCT
1441 -----+-----+-----+-----+-----+-----+ 1500
TGGAACCGGAGAGGAACCTCCTGGAATCCAGTTTGAGGGATCAGAGGTGGACTCTGGGA
GGGAGAGAAGTTTGAAGCACAACTCCCTTAAGGTCTCCAAACCAGACGGTGACGCCTGCG
1501 -----+-----+-----+-----+-----+-----+ 1560
CCCTCTCTTCAAACCTCGTGTGAGGGAATTCAGAGGTTGGTCTGCCACTGCGGACGC
GGACCATCTGGGGCACCTGCTTCCACCCGTCTCTCTGCCACTCGGGTCTGCAGACCTGG
1561 -----+-----+-----+-----+-----+-----+ 1620
CCTGGTAGACCCCGTGACGAAGGTGGGCAGAGAGCGGTGAGCCAGACGTCTGGACC
TTCCCACTGAGGCCCTTTCAGGATGGAACCTACGGGGCTTACAGGAGCTTTTGTGTGCCT
1621 -----+-----+-----+-----+-----+-----+ 1680
AAGGGTGACTCCGGGAACGTCTACCTTGATGCCCGAATGTCTCGAAAACACACGGA
GGTAGAACTATTTCTGTTCAGTCACATTGCCATCACTCTGTACTGCCTGCCACCGCG
1681 -----+-----+-----+-----+-----+-----+ 1740
CCATCTTTGATAAAGACAAGGTCAGTGTAAACGGTAGTGAGAACATGACGGACGGTGGCGC
GAGGAGGCTGGTGACAGGCCAAAGGCCAGTGGAAGAAACACCCCTTCATCTCAGAGTCCA
1741 -----+-----+-----+-----+-----+-----+ 1800
CTCCTCCGACCACTGTCCGGTTTCCGGTCTCTTCTTTGTGGAAAGTAGAGTCTCAGGT
CTGTGGCACTGGCCACCCCTCCCCAGTACAGGGTGTCTGCAGGTGGCAGAGTGAATGTCC
1801 -----+-----+-----+-----+-----+-----+ 1860
GACACCGTGACCGGTGGGGAGGGGTCTGTCTCCACGACGTCCACCGTCTCACTTACAGG
CCCATCATGTGGCCCAACTCTCCTGGCCTGGCCATCTCCCTCCCCAGAAACAGTGTGCAT
1861 -----+-----+-----+-----+-----+-----+ 1920
GGGTAGTACACCGGGTTGAGAGGACCGGACCGGTAGAGGGAGGGTCTTTGTACACGTA
GGGTTATTTTGGAGTGTAGGTGACTTGTCTTACTCATTGAAGCAGATTTCTGCTTCCTTTT
1921 -----+-----+-----+-----+-----+-----+ 1980
CCCAATAAAACCTCACATCCACTGAACAAATGAGTAACCTTCGTCTAAGACGAAGGAAAA
ATTTTTATAGGAATAGAGGAAGAAATGTCAGATGCGTGCCAGCTCTTCACCCCCAATC
1981 -----+-----+-----+-----+-----+-----+ 2040
TAAAAATATCCTTATCTCCTTCTTACAGTCTACGCACGGGTGAGAAAGTGGGGGGTTAG

FIG. 1C

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2041 TCTTGGTGGGGAGGGGTGTACCTAAATATTATCATATCCTTGCCCTGAGTGCTTGTTA
-----+-----+-----+-----+-----+ 2100
AGAACCACCCCTCCCCACATGGATTATATAATAGTATAGGAACGGGAACACGAACAAT

2101 GAGAGAAAGAGAACTACTAAGGAAAATAATATTATTAACTCGCTCCTAGTGTTTCTTT
-----+-----+-----+-----+-----+ 2160
CTCTCTTTCTCTTGATGATTCTTTTATTATAATAAATTGAGCGAGGATCACAAGAAA

2161 GTGGTCTGTGTACCGTATCTCAGGAAGTCCAGCCACTTGACTGGCACACACCCCTCCGG
-----+-----+-----+-----+-----+ 2220
CACCAGACACAGTGGCATAGAGTCTTCAGGTCGGTGAACGACCGTGTGTGGGGAGGCC

2221 ACATCCAGCGTGACGGAGCCCACTGCCACCTTGTGGCCGCTGAGACCTCGCGCCCC
-----+-----+-----+-----+-----+ 2280
TGTAGGTCGCACTGCCTCGGGTGTGACGGTGGAAACACCGCGGACTCTGGGAGCGCGGG

2281 CCGCGCCCCCGCGCCCTCTTTTCCCTTGATGGAAATTGACCATACAATTCATCCT
-----+-----+-----+-----+-----+ 2340
GGCGCGGGGGCGCGGGGAGAAAAGGGGAACCTCTTAAGTGGTATGTTAAGTAGGA

2341 CCTTCAGGGGATCAAAGGACGGAGTGGGGGGACAGAGACTCAGATGAGGACAGAGTGGT
-----+-----+-----+-----+-----+ 2400
GGAAGTCCCCTAGTTTCTGCTCAGCCCCCTGTCTGTGAGTCTACTCCTGTCTACCA

2401 TTCCAATGTGTTCAATAGATTTAGGAGCAGAAATGCAAGGGGCTGCATGACCTACCAGGA
-----+-----+-----+-----+-----+ 2460
AAGGTTACACAAGTTATCTAAATCCTCGTCTTTACGTTCCCGACGTACTGGATGGTCCT

2461 CAGAACTTTCCCAATTACAGGGTGACTCACAGCCGCTTGGTGACTCACTTCAATGTGT
-----+-----+-----+-----+-----+ 2520
GTCTTGAAAGGGGTTAATGTCCCACTGAGTGTGCGCGTAACCACTGAGTGAAGTTACACA

2521 CATTTCCGGCTGCTGTGTGTGAGCAGTGGACACGTGAGGGGGGGTGGGTGAGAGAGACA
-----+-----+-----+-----+-----+ 2580
GTAAAGGCCGACGACACACTCGTCACCTGTGCACTCCCCCCCCACCACTCTCTCTGT

2581 GGCAGCTCGGATTCAACTACCTTAGATAATATTCTGAAAACCTACCAGCCAGAGGGTAG
-----+-----+-----+-----+-----+ 2640
CCGTCGAGCCTAAGTTGATGGAATCTATTATAAAGACTTTGGATGGTCGGTCTCCCATC

2641 GGCACAAAGATGGATGTAATGCACCTTGGGAGGCCAAGGCGGGAGGATTGCTTGAGCCCA
-----+-----+-----+-----+-----+ 2700
CCGTGTTTCTACCTACATTACGTGAAACCTCCGGTTCGCCCCCTCTAACGAACCTCGGGT

2701 GGAGTTCAAGACCAGCCTGGGCAACATACCAAGACCCCGTCTCTTAAAAATATATATA
-----+-----+-----+-----+-----+ 2760
CCTCAAGTTCTGGTCCGACCCGTTGTATGGTTCGGGGGAGAGAAATTTTATATATAT

2761 TTTTAAATATACTTAAATATATATTCTAATATCTTTAAATATATATATATTTTAAAG
-----+-----+-----+-----+-----+ 2820
AAAATTTATATGAATTTATATATAAAGATTATAGAAATTTATATATATATATAAATTC

2821 ACCAATTTATGGGAGAATTGCACACAGATGTGAAATGAATGTAATCTAATAGAAGC
-----+-----+-----+-----+-----+ 2876
TGGTTAAATACCCTCTTAACGTGTGTCTACACTTTACTTACATTAGATTATCTTCG

FIG. 1D

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MQMSPALTCLVLGLALVFGECSA
Signal peptide

VHHPFSYVAHLASDFGVRVFQOVAQASKDRNVVFSPIGVASVLAMLQLTTGGETQQQIQ
AMGFKIDDKGMAPALRHLYKELMGFWNKDEISTDAIFVQDLKLVQGFMPHFFRLFRST
VKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP
DSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDLSMFIAAP
YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR
QFQADFTSLSDQEPLHVAQALQVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFLF
VVRHNPTGTVLFMQVMEP

FIG. 2A

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10 20 30 40 50 60
VHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPIGVASVLAMLQTTGGETQQQIQ

70 80 90 100 110 120
AMGFKIDDKGMAPALRHLYKELMGPNKDEISTDAIFVQDLKLVOGFMPHFFRLFRST

130 140 150 160 170 180
VKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP

190 200 210 220 230 240
DSSTHRRFLFKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDLSMFIAAP

250 260 270 280 290 300
YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR

310 320 330 340 350 360
QFQADFTSLSDQEPLHVAQALQVKIEVNESGTVASSSTAVIVSARMAPEEIIIMDRPFLF

370
VVRHNPTGTVLFMGQVMEP

FIG. 2B

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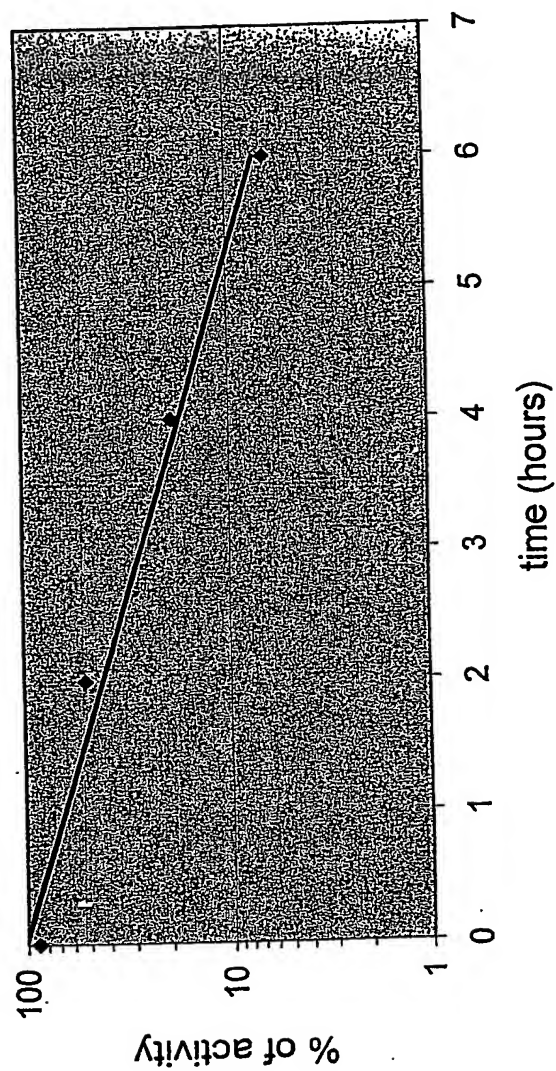


FIG. 3

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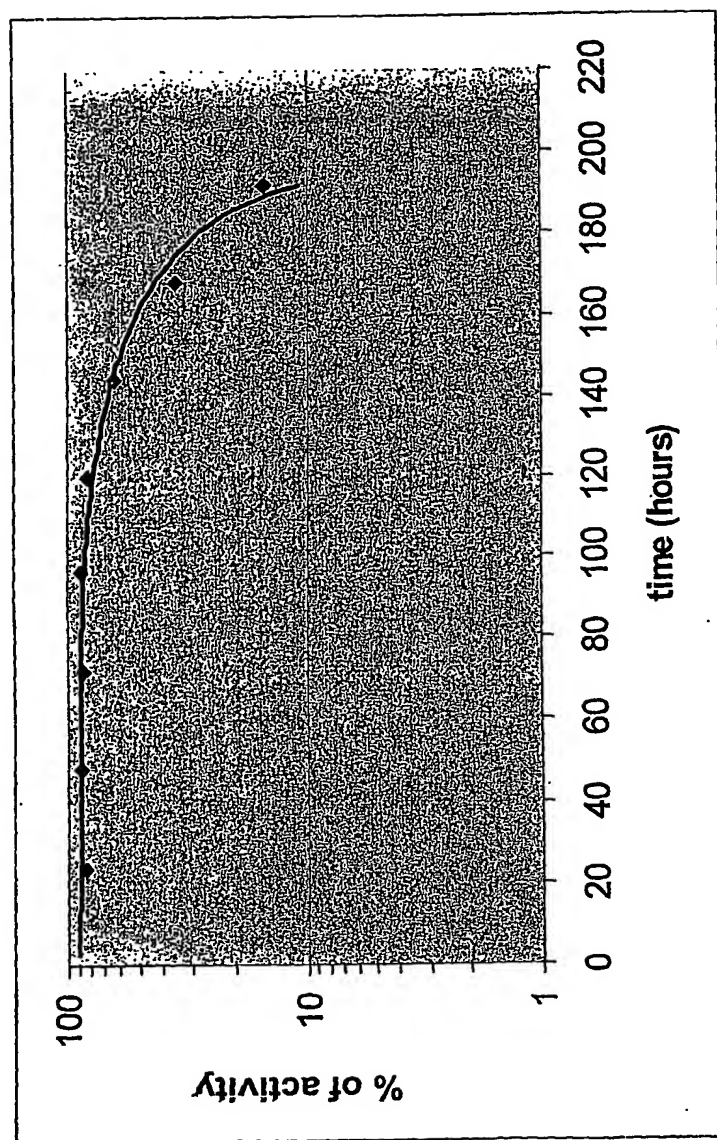


FIG. 4

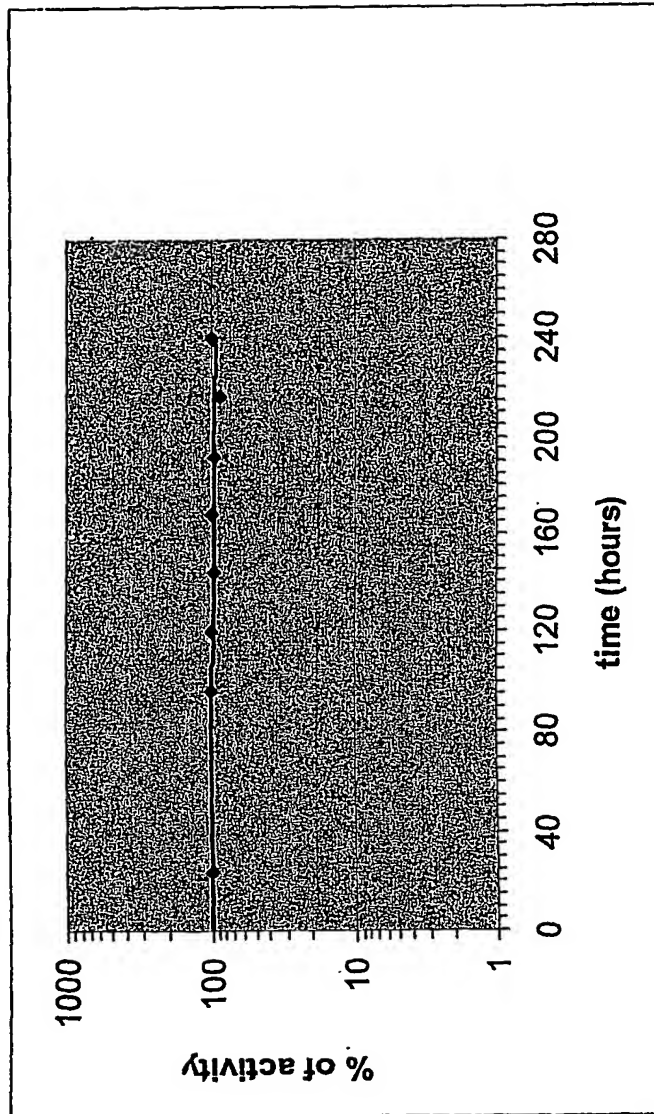


FIG. 5

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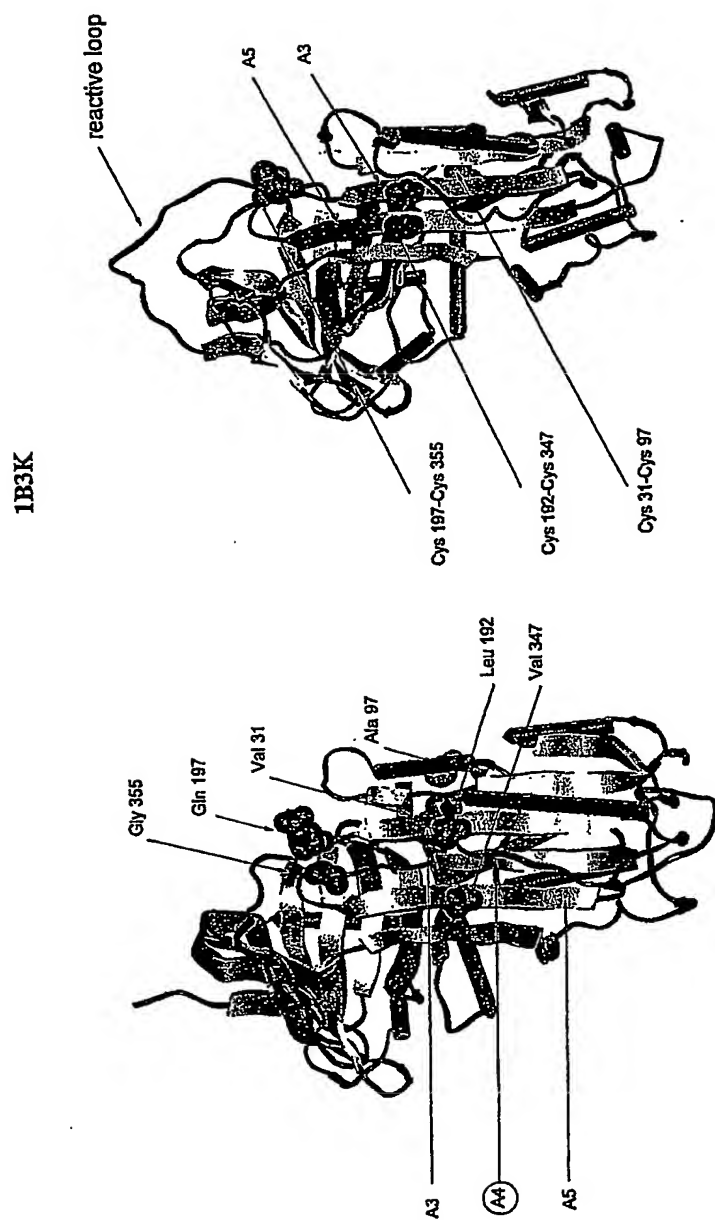


FIG. 6

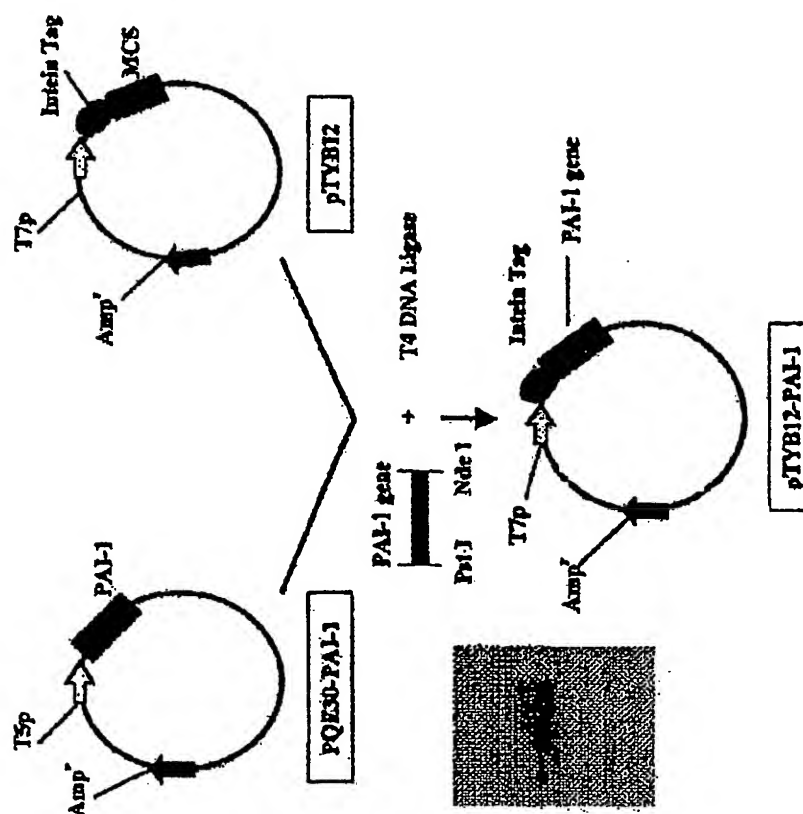


FIG. 7

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FIG. 8B

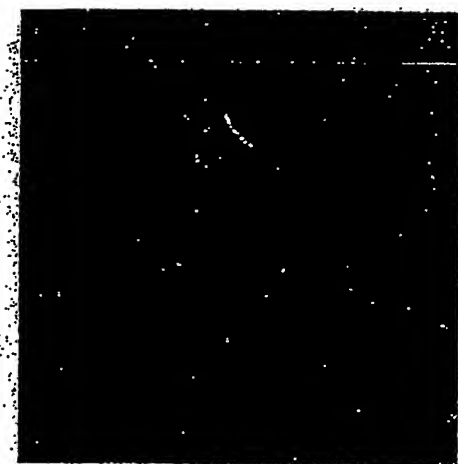


FIG. 8A

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FIG. 9B



FIG. 9A

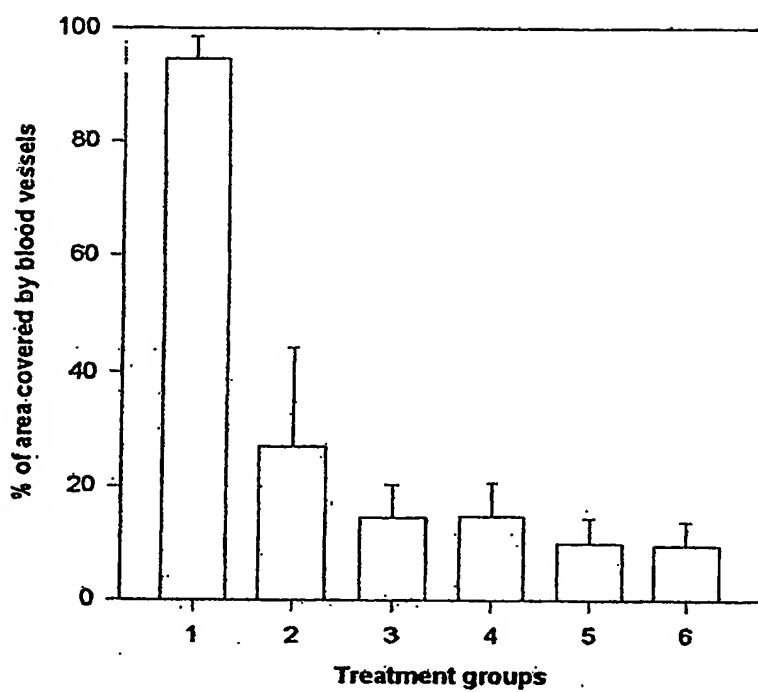


FIG. 10

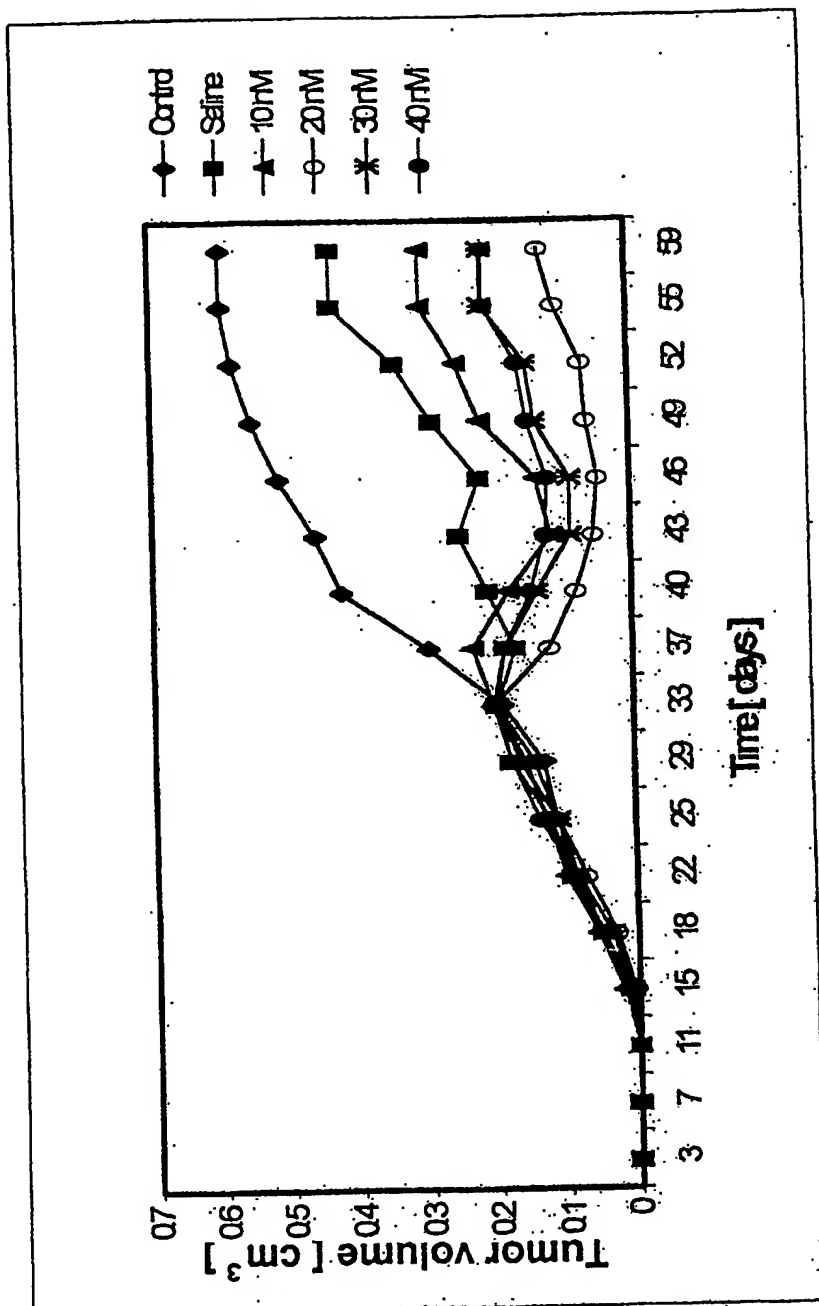


FIG. 11

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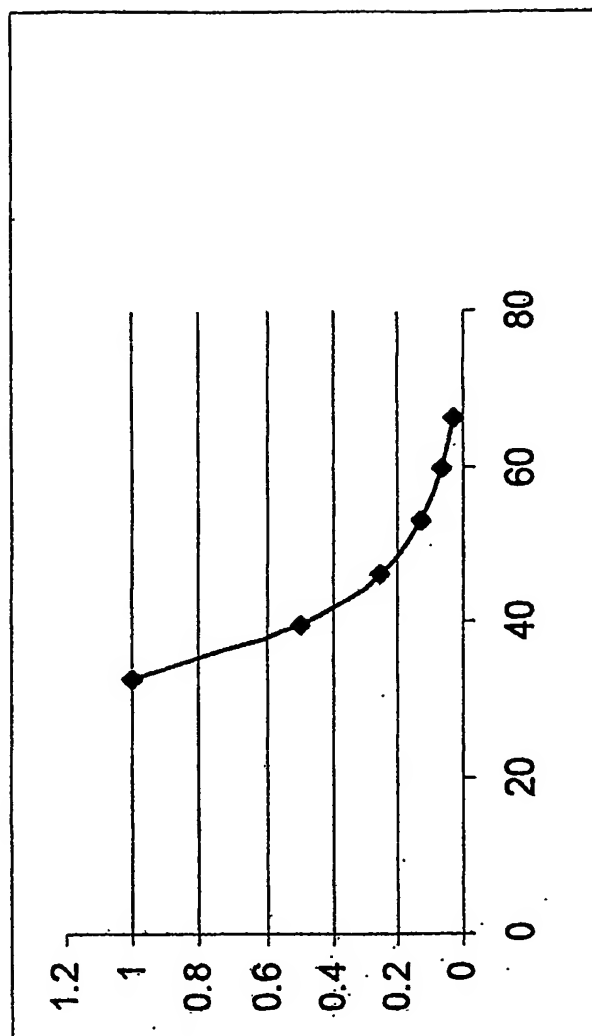


FIG. 12

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